n=37,630 sequenced genomes, from 1 March 2025 up to 10 June 2025

Global

- ●JN.1.* +DeFLuQE ●JN.1.* +FLiRT ●LP.8.1.* ●NB.1.8.1.* Nimbus ●XEC.* ●XFG.*



Lineage Frequency

40%

30%

20%

10%

0%

Mar 2025    Apr 2025    May 2025    Jun 2025

samples (n)

0

500

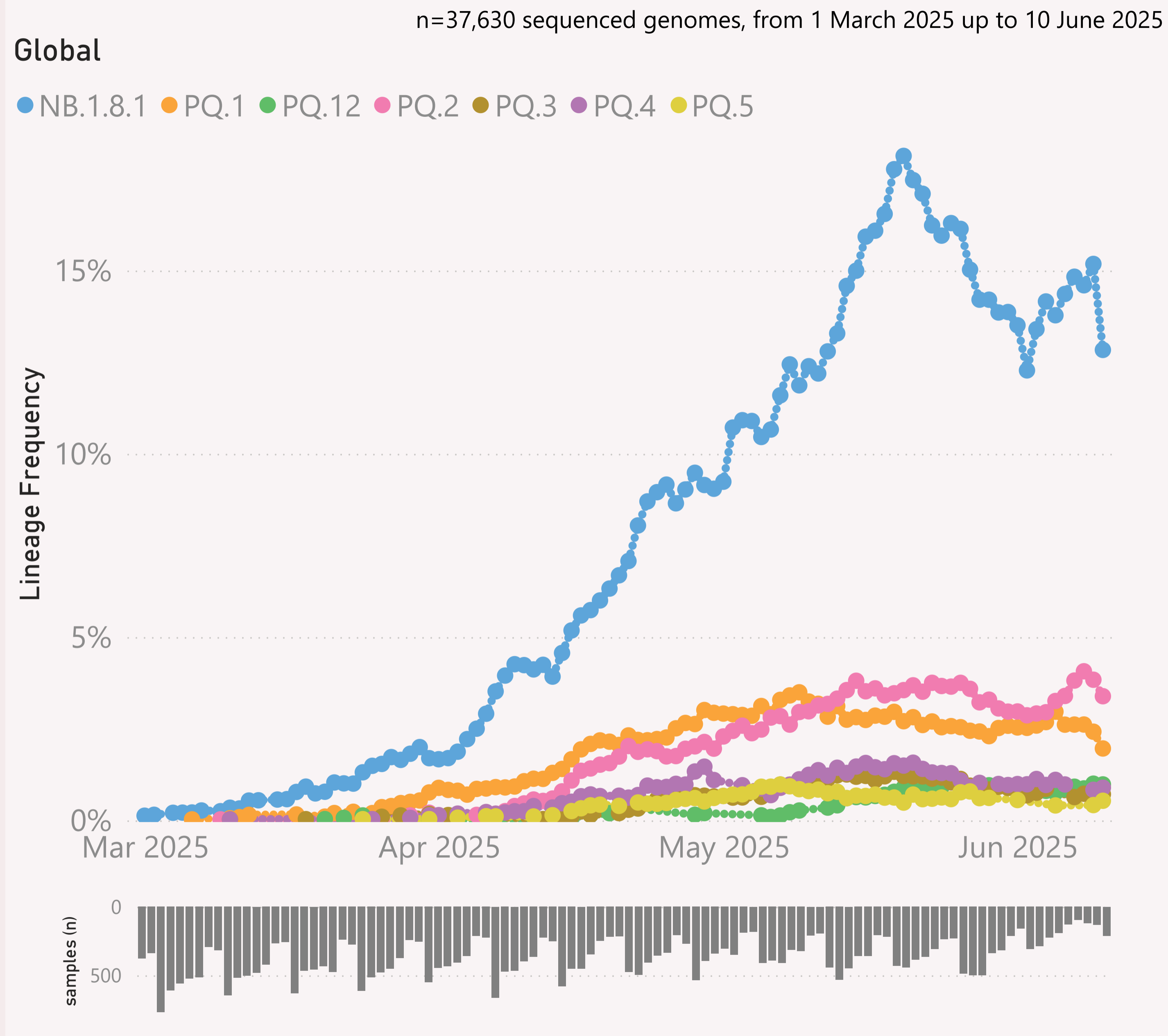This page shows the frequency of the top 6 "L2" lineages, across recent months.

The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "BA.2.86.*" group includes BA.2.86 and all it's descendants, e.g. the JN.* lineages.

The detailed Lineage classifications are quite numerous and dynamic, so the "Lineage L2" groups give a simpler and more stable basis for analysis and comparison.

The frequency shown at each point is based on the 7-day rolling average across all lineages.

The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

The frequency results calculated for the most recent dates might not be representative, due to those lower sample sizes.

n=37,630 sequenced genomes, from 1 March 2025 up to 10 June 2025

**Global**

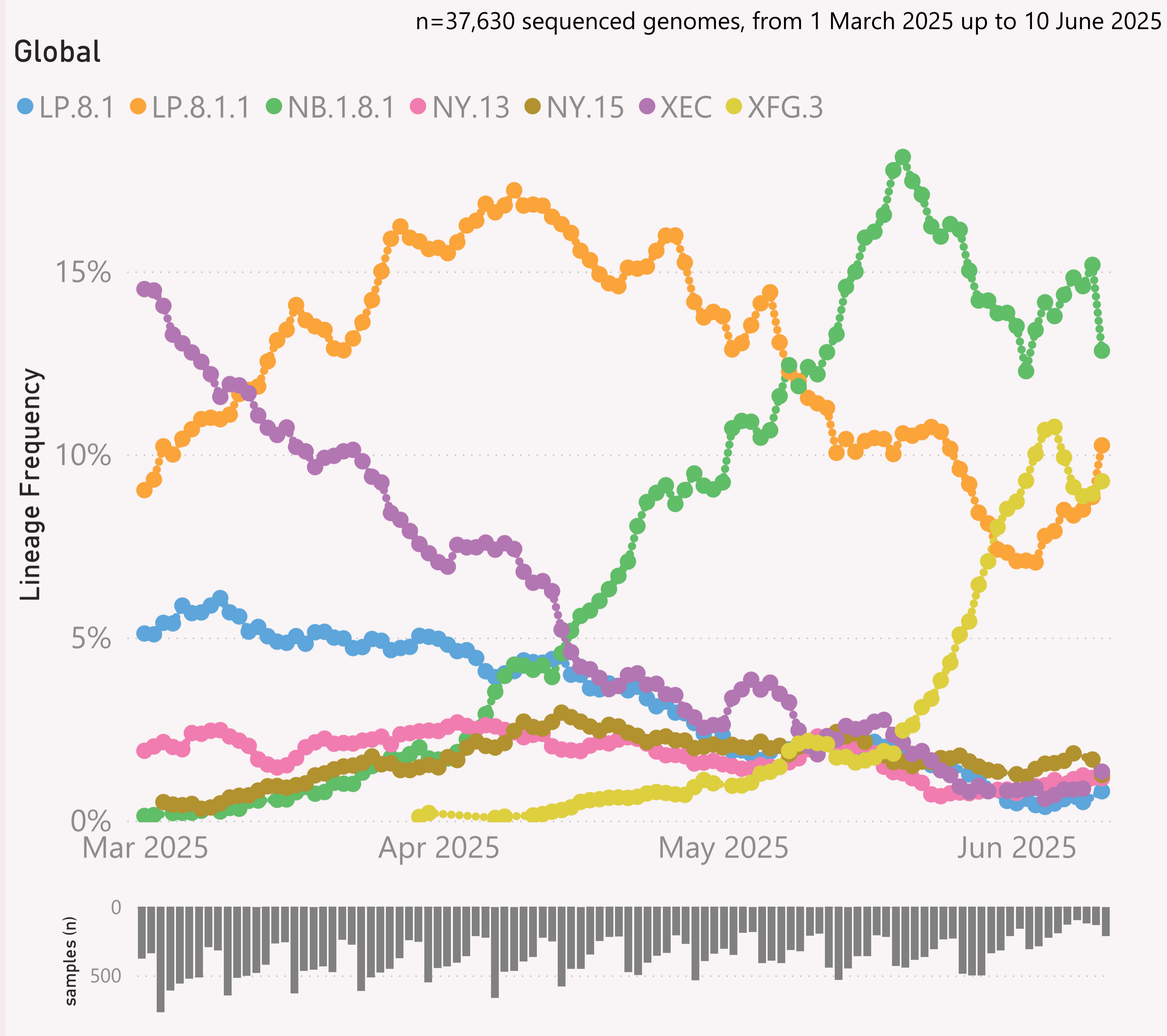● NB.1.8.1   ● PQ.1   ● PQ.12   ● PQ.2   ● PQ.3   ● PQ.4   ● PQ.5



This page shows the frequency of the top 7 lineages, across recent months. The lineages are filtered for a "Lineage L2" group of interest, currently NB.1.8.1.* Nimbus.

The Lineage classifications are provided by Nextclade. The colour assignments are random.

The frequency shown at each point is based on the 7-day rolling average across all lineages.

The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

The frequency results calculated for the most recent dates might not be representative, due to those lower sample sizes.

n=37,630 sequenced genomes, from 1 March 2025 up to 10 June 2025



Global

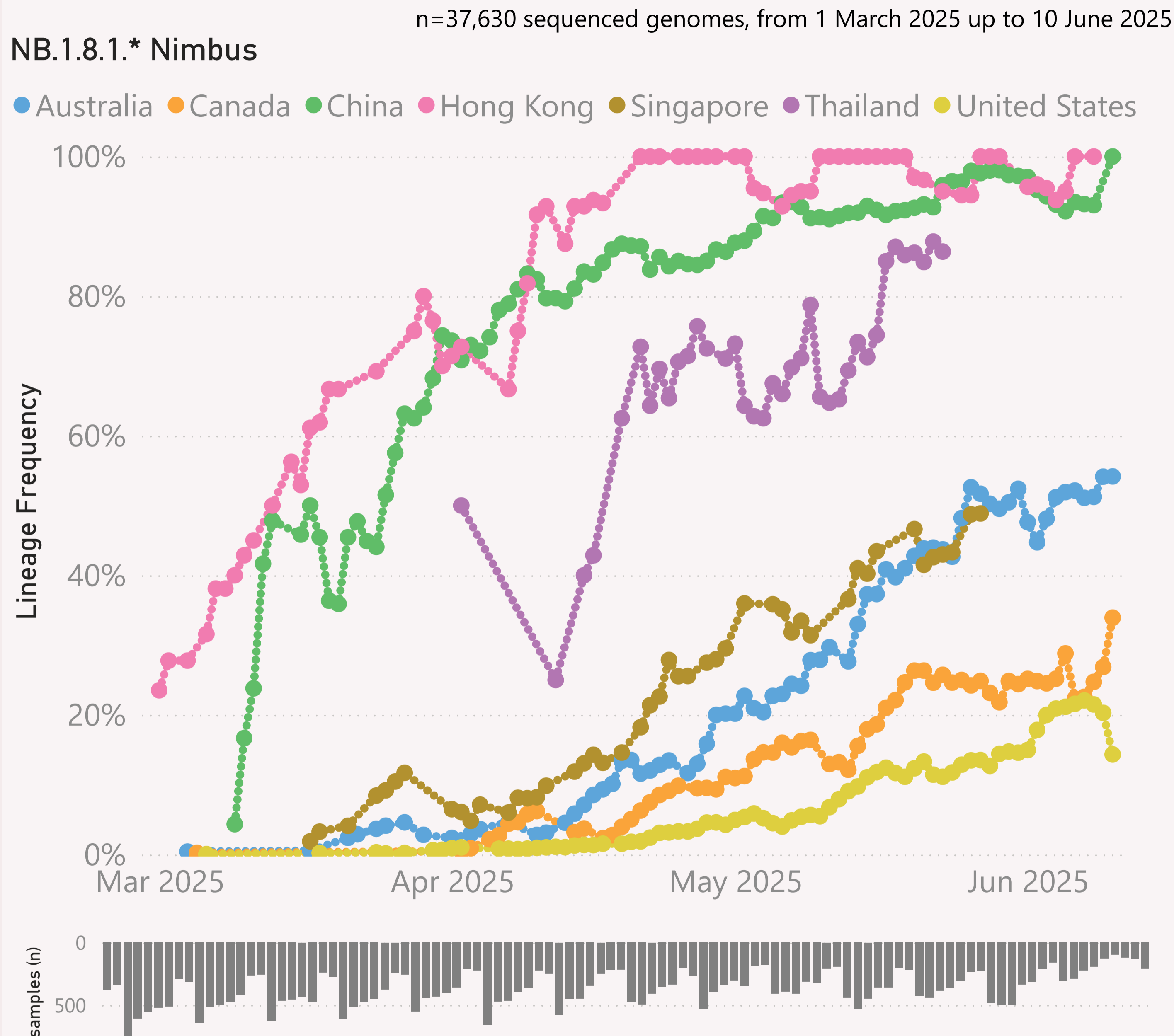LP.8.1 ● LP.8.1.1 ● NB.1.8.1 ● NY.13 ● NY.15 ● XEC ● XFG.3

This page shows the frequency of the top 7 lineages, across recent months.

The Lineage classifications are provided by Nextclade. The colour assignments are random.

The frequency shown at each point is based on the 7-day rolling average across all lineages.

The grey column chart across the bottom shows the volume of sequences available by date.  As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

The frequency results calculated for the most recent dates might not be representative, due to those lower sample sizes.

n=37,630 sequenced genomes, from 1 March 2025 up to 10 June 2025

NB.1.8.1.* Nimbus

● Australia ● Canada ● China ● Hong Kong ● Singapore ● Thailand ● United States

This page shows the frequency of a selected "Lineage L2" group of interest, for the 7 countries reporting the most samples over recent months.
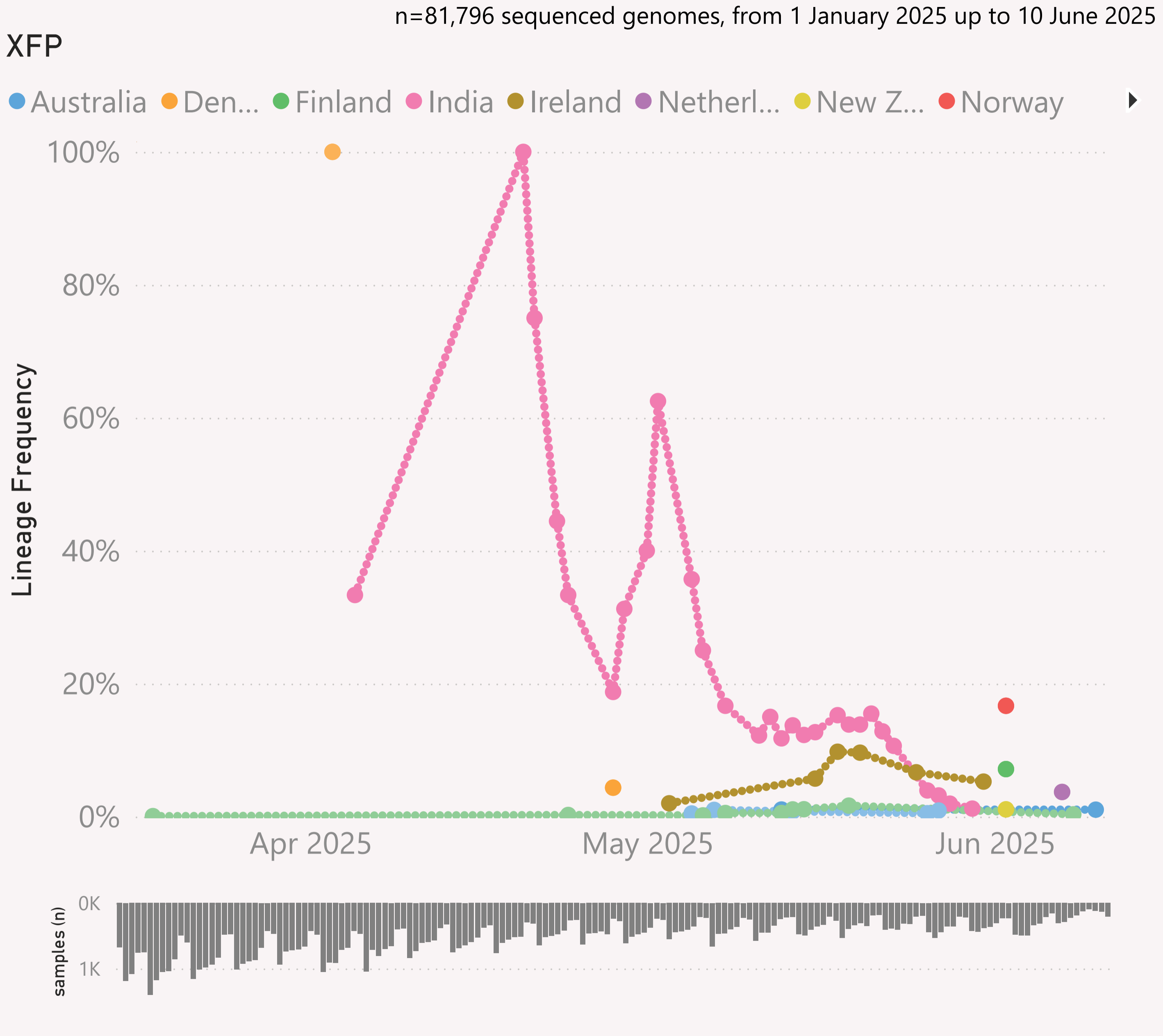
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "JN.1.* +FLiRT" group includes the descendants of JN.1.* with the mutations: F456L & R346T.

The detailed Lineage classifications are quite numerous and dynamic, so the "Lineage L2" groups give a simpler and more stable basis for analysis and comparison.

The frequency shown at each point is based on the 7-day rolling average across all lineages, for that country.

The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

The frequency results calculated for the most recent dates might not be representative, due to those lower sample sizes.

n=37,630 sequenced genomes, from 1 March 2025 up to 10 June 2025

XFG.*

- Australia
- Canada
- France
- India
- Spain
- United Kingdom
- United States



This page shows the frequency of a selected "Lineage L2" group of interest, for the 7 countries reporting the most samples over recent months.

The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "JN.1.* +FLiRT" group includes the descendants of JN.1.* with the mutations: F456L & R346T.

The detailed Lineage classifications are quite numerous and dynamic, so the "Lineage L2" groups give a simpler and more stable basis for analysis and comparison.

The frequency shown at each point is based on the 7-day rolling average across all lineages, for that country.

The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

The frequency results calculated for the most recent dates might not be representative, due to those lower sample sizes.

n=81,796 sequenced genomes, from 1 January 2025 up to 10 June 2025

## XFP

- Australia
- Den...
- Finland
- India
- Ireland
- Netherl...
- New Z...
- Norway



**Date**

01/01/2025   31/12/2025

**Host**

Human

**Continent, Country, Location**

All

**Lineage L2, Lineage (nextclade)**

XFP.* (Lineage L2) + XFP (Lineage (nextclad...

**# Samples Sequenced (gisaid)**

75

| Country | Location | Addi... | Collection date | Lineage L2 | Lineage (nextc... |
|---------|----------|---------|-----------------|------------|--------|
| Australia | Western Austr... | | 10/06/2025 | XFP.* | XFP |
| USA | International Tr... | | 08/06/2025 | XFP.* | XFP |
| Netherlands | Gelderland | | 07/06/2025 | XFP.* | XFP |
| Finland | | | 02/06/2025 | XFP.* | XFP |
| New Zealand | Southern | | 02/06/2025 | XFP.* | XFP |
| Norway | Vestland | | 02/06/2025 | XFP.* | XFP |
| Ireland | Dublin | | 31/05/2025 | XFP.* | XFP |
| India | Maharashtra | | 30/05/2025 | XFP.* | XFP |
| India | Madhya Pradesh | | 28/05/2025 | XFP.* | XFP |
| India | Maharashtra | Othe... | 28/05/2025 | XFP.* | XFP |
| Singapore | | | 27/05/2025 | XFP.* | XFP |
| India | Andhra Pradesh | | 27/05/2025 | XFP.* | XFP |
| Singapore | | | 26/05/2025 | XFP.* | XFP |
| India | Gujarat | | 26/05/2025 | XFP.* | XFP |
| Ireland | Dublin | | 25/05/2025 | XFP.* | XFP |
| India | Karnataka | | 23/05/2025 | XFP.* | XFP |
| India | Gujarat | | 22/05/2025 | XFP.* | XFP |
| India | Maharashtra | Othe... | 21/05/2025 | XFP.* | XFP |
| India | Tamil Nadu | | 21/05/2025 | XFP.* | XFP |
| Ireland | Dublin | | 20/05/2025 | XFP.* | XFP |
| India | Tamil Nadu | | 20/05/2025 | XFP.* | XFP |
| USA | International Tr... | | 19/05/2025 | XFP.* | XFP |

**Total**

n=23,755 sequenced genomes, from 1 April 2025 up to 10 June 2025

## Global – NB.1.8.1.* Nimbus vs LP.8.1.*

● log ( 1st Lineage / 2nd Lineage )   ● trend

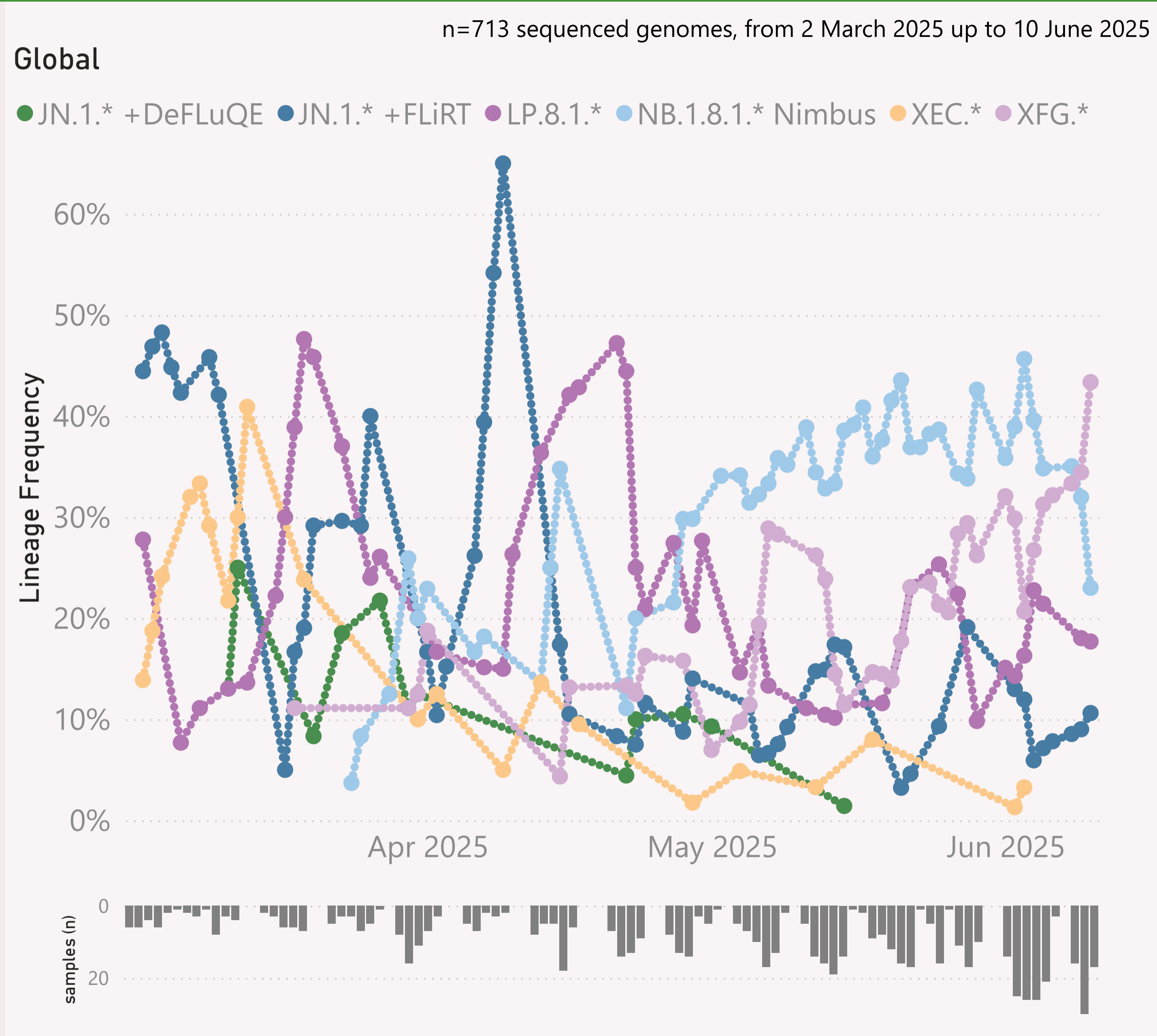growth of 3.3% per day, crossover on 24-May-25



This page compares the relative frequency of 2 selected "Lineage L2" groups, over recent months. A challenging Lineage L2 is selected first, and compared to the incumbent.

The trend is shown as a green line and expressed as a daily growth % advantage. If the green line crosses over the 0.0 line, the date when that occurred or is predicted to occur will be shown. At that point the challenging Lineage L2 is considered to have "crossed over" or taken over dominance from the incumbent Lineage L2.

The Lineage classifications are provided by Nextclade. I add the "Lineage L2" groups, typically following common variant groupings, but occasionally being "creative".

The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

n=23,755 sequenced genomes, from 1 April 2025 up to 10 June 2025

## Global – XFG.* vs LP.8.1.*

● log ( 1st Lineage / 2nd Lineage )   ● trend

growth of 6.3% per day, crossover on 02-Jun-25



This page compares the relative frequency of 2 selected "Lineage L2" groups, over recent months. A challenging Lineage L2 is selected first, and compared to the incumbent.

The trend is shown as a green line and expressed as a daily growth % advantage. If the green line crosses over the 0.0 line, the date when that occurred or is predicted to occur will be shown. At that point the challenging Lineage L2 is considered to have "crossed over" or taken over dominance from the incumbent Lineage L2.

The Lineage classifications are provided by Nextclade. I add the "Lineage L2" groups, typically following common variant groupings, but occasionally being "creative".

The grey column chart across the bottom shows the volume of sequences available by date.  As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

n=23,755 sequenced genomes, from 1 April 2025 up to 10 June 2025

## Global - XFP vs LP.8.1.1

● log ( 1st Lineage / 2nd Lineage )   ● trend

0 ·········································································································

growth of 2.3% per day
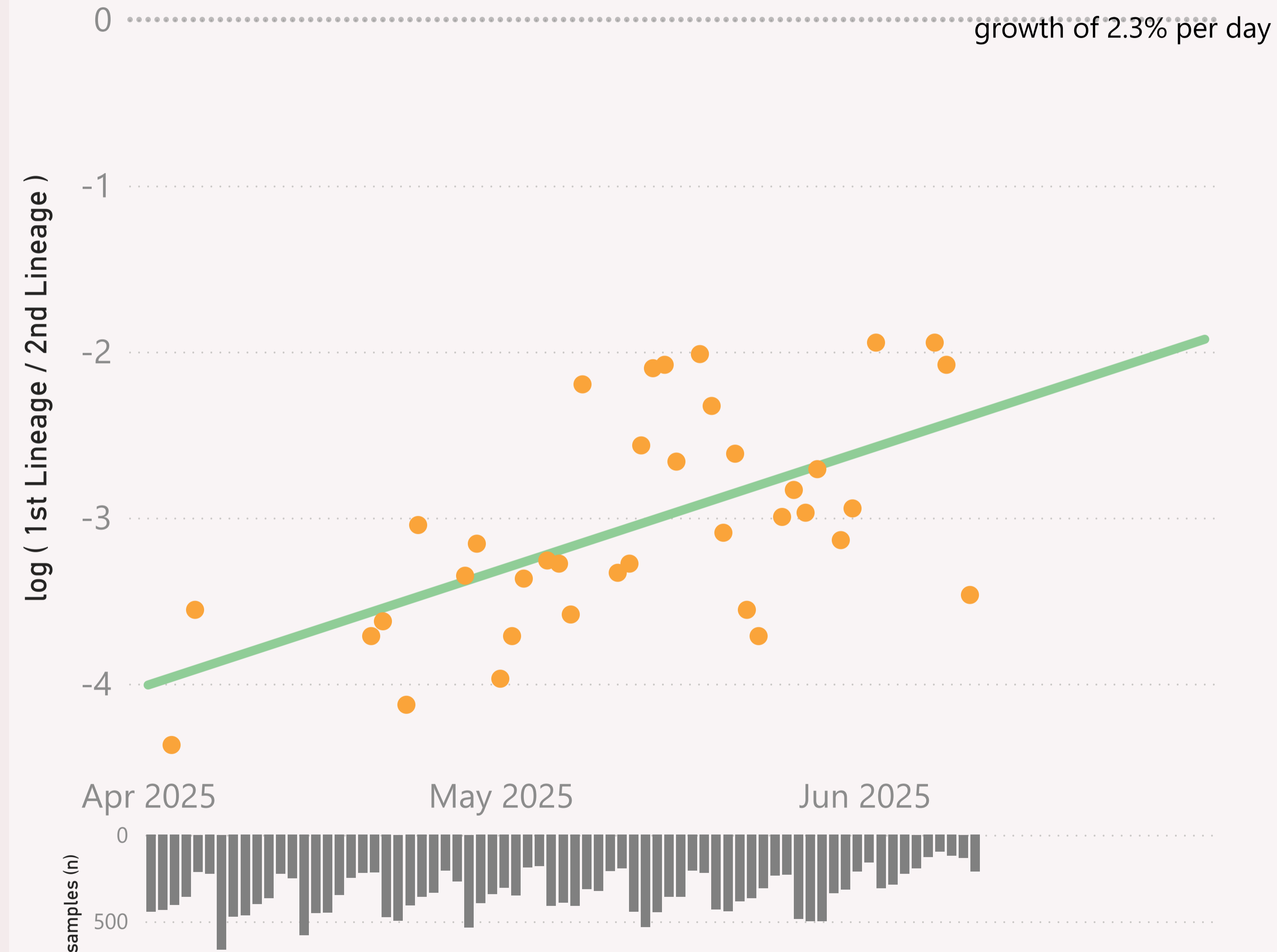


This page compares the relative frequency of 2 selected Lineages, over recent months. A challenging Lineage is selected first, and compared to the incumbent.

The trend is shown as a green line and expressed as a daily growth % advantage. If the green line crosses over the 0.0 line, the date when that occurred or is predicted to occur will be shown. At that point the challenging Lineage is considered to have "crossed over" or taken over dominance from the incumbent Lineage

The Lineage classifications are provided by Nextclade.

The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

n=37,630 sequenced genomes, from 1 March 2025 up to 10 June 2025
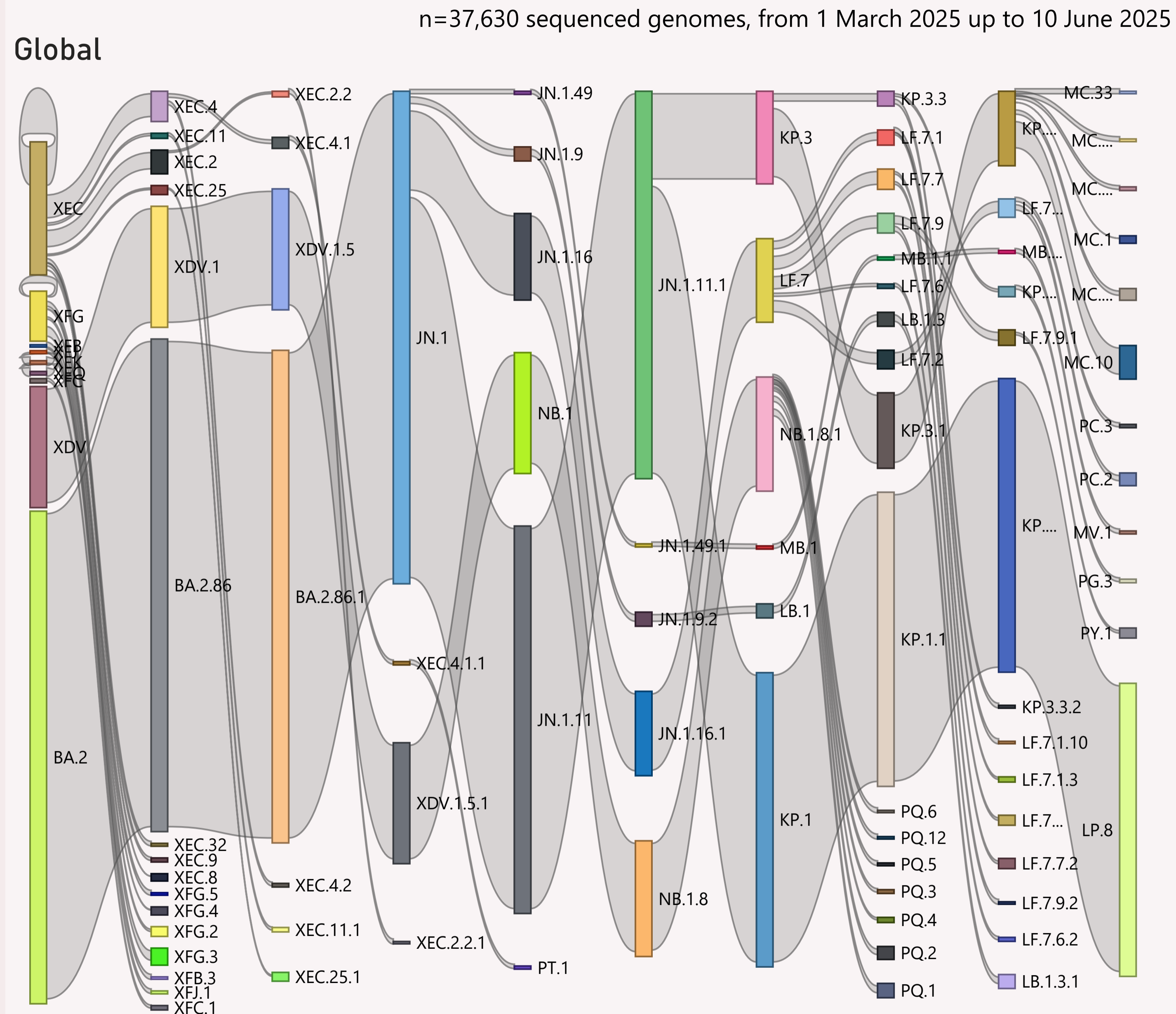


This page shows the hierarchy of the significant Lineages, over recent months.

The hierarchy can be read from left to right, starting with the earliest/highest Lineages being broken down into more detailed child Lineages.

The vertical height of each bar segment represents the relative volume of all the samples of that specific Lineage, as well as all it's descendants.

The full picture is typically quite busy, so insignificant Lineages (with few samples, or at the extreme top or bottom of the hierarchy) are not shown.

The Lineage classifications are provided by Nextclade.

COVID-19 Genomic Sequencing analysis - International Travellers only. Data from gisaid.org, with nextclade lineages. Source files and more info on github.     Last Update: 2025-06-28 12:25 (UTC)

n=713 sequenced genomes, from 2 March 2025 up to 10 June 2025

**Global**

● JN.1.* +DeFLuQE  ● JN.1.* +FLiRT  ● LP.8.1.*  ● NB.1.8.1.* Nimbus  ● XEC.*  ● XFG.*
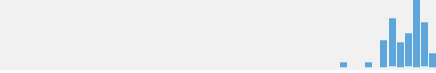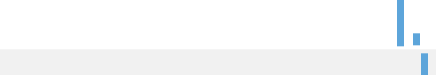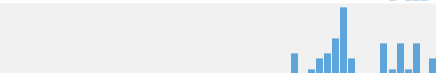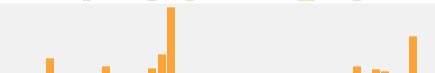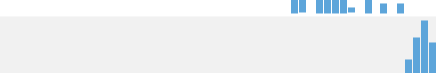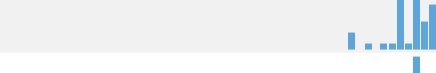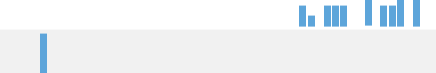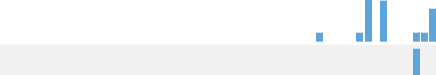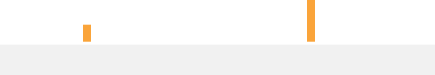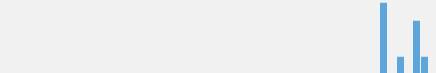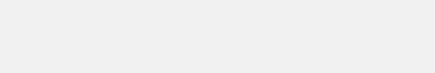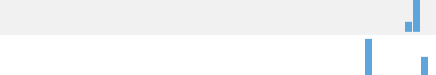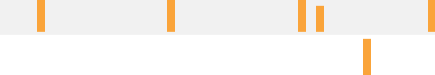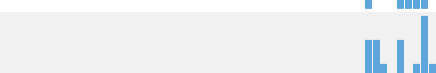
This page shows the frequency of the top 6 "L2" lineages, across recent months, for "International Traveller" samples.

This is probably a more randomised sample than the "Global" aggregate of all samples submitted to GISAID, as those are dominated by the US and Canada

These samples are mainly collected from arrivals into the US and Japan.

## Data Submitted in the last 8 weeks

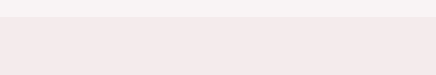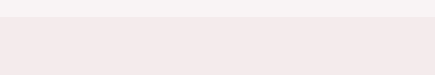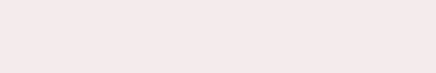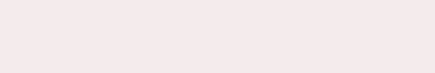| Country | # Samples Sequenced | Latest Collection date | by Collection date | Latest Submission date | by Submission date |
|---|---|---|---|---|---|
| ⊞ Canada | 25,284 | 10/06/2025 | | 22/06/2025 | |
| ⊞ United States | 9,403 | 10/06/2025 | | 22/06/2025 | |
| ⊞ China | 2,085 | 10/06/2025 | | 22/06/2025 | |
| ⊞ Spain | 1,583 | 10/06/2025 | | 22/06/2025 | |
| ⊞ United Kingdom | 1,518 | 10/06/2025 | | 22/06/2025 | |
| ⊞ Australia | 1,238 | 10/06/2025 | | 22/06/2025 | |
| ⊞ Singapore | 1,029 | 27/05/2025 | | 02/06/2025 | |
| ⊞ India | 807 | 05/06/2025 | | 22/06/2025 | |
| ⊞ France | 774 | 10/06/2025 | | 18/06/2025 | |
| ⊞ Japan | 744 | 10/06/2025 | | 22/06/2025 | |
| ⊞ Brazil | 688 | 04/06/2025 | | 22/06/2025 | |
| ⊞ Mexico | 549 | 19/05/2025 | | 12/06/2025 | |
| ⊞ Russia | 440 | 12/05/2025 | | 21/06/2025 | |
| ⊞ New Zealand | 430 | 10/06/2025 | | 22/06/2025 | |
| ⊞ South Korea | 419 | 04/06/2025 | | 22/06/2025 | |
| ⊞ Ireland | 349 | 10/06/2025 | | 22/06/2025 | |
| ⊞ Malaysia | 312 | 09/06/2025 | | 20/06/2025 | |
| ⊞ Kazakhstan | 303 | 28/05/2025 | | 20/06/2025 | |
| ⊞ Thailand | 281 | 23/05/2025 | | 30/05/2025 | |
| ⊞ Italy | 184 | 07/06/2025 | | 22/06/2025 | |
| ⊞ Norway | 184 | 10/06/2025 | | 22/06/2025 | |
| ⊞ Portugal | 177 | 03/06/2025 | | 22/06/2025 | |
| ⊞ Netherlands | 175 | 09/06/2025 | | 22/06/2025 | |
| ⊞ Luxembourg | 171 | 02/06/2025 | | 19/06/2025 | |
| ⊞ Germany | 168 | 10/06/2025 | | 22/06/2025 | |
| ⊞ Hong Kong | 154 | 08/06/2025 | | 22/06/2025 | |
| ⊞ Costa Rica | 134 | 05/06/2025 | | 22/06/2025 | |
| ⊞ Sweden | 133 | 10/06/2025 | | 22/06/2025 | |
| **Total** | **51,221** | **10/06/2025** | | **22/06/2025** | |

This page shows the volume and currency/timeliness of the genomic sequencing data shared via GISAID, over the last 8 weeks, for the countries sharing the most samples.

Each sample shared comes with a Collection date - when the PCR test for that sample was collected. The GISAID system also records a Submission date for each sample, which is typically the date that sample was uploaded.

The latest date of each type is shown, along with "sparkline"-style mini charts to give a flavour for the spread of recent data by Collection date and by Submission date.